

# Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

## PARASAIL

RRID:SCR\_021805

Type: Tool

### Proper Citation

PARASAIL (RRID:SCR\_021805)

### Resource Information

**URL:** <https://github.com/jeffdaily/parasail>

**Proper Citation:** PARASAIL (RRID:SCR\_021805)

**Description:** Software tool as multiple sequence alignment for global, local and semi global alignments.

**Synonyms:** Pairwise Sequence Alignment Library

**Resource Type:** alignment software, data processing software, image analysis software, software application, software resource

**Defining Citation:** [DOI:10.1186/s12859-016-0930-z](https://doi.org/10.1186/s12859-016-0930-z)

**Keywords:** multiple sequence alignment, global alignments, local alignments, semi global alignments,

**Funding:** Pacific Northwest National Laboratory

**Availability:** Free, Available for download, Freely available

**Resource Name:** PARASAIL

**Resource ID:** SCR\_021805

**Alternate URLs:** <https://sources.debian.org/src/libparasail-dev/>

**License:** Battelle BSD-style

**License URLs:** <https://github.com/jeffdaily/parasail/blob/master/LICENSE.md>

**Record Creation Time:** 20220129T080357+0000

**Record Last Update:** 20260912T200002+0000

---

## Ratings and Alerts

No rating or validation information has been found for PARASAIL.

No alerts have been found for PARASAIL.

---

## Data and Source Information

**Source:** [SciCrunch Registry](#)

---

## Usage and Citation Metrics

We found 4 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [SPARC SAWG](#) .

Bonab RR, et al. (2025) SW-actors: accelerating the Smith-Waterman algorithm via actors. Bioinformatics advances, 5(1), vbaf173.

Luo H, et al. (2025) Large-Scale T-cell Receptor Repertoire Profiling Unveils Tumor-Specific Signals for Diagnosing Indeterminate Pulmonary Nodules. Cancer research, 85(24), 5141.

Zong P, et al. (2024) TSTA: thread and SIMD-based trapezoidal pairwise/multiple sequence-alignment method. GigaByte (Hong Kong, China), 2024, gigabyte141.

Vanni C, et al. (2022) Unifying the known and unknown microbial coding sequence space. eLife, 11.